\_\_\_\_\_\_

Sequence Listing could not be accepted.

If you need help call the Patent Electronic Business Center at (866)

217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: Thu May 03 16:48:36 EDT 2007

\_\_\_\_\_

Reviewer Comments:

<210> 4

<211> 6223

<212> DNA

<213> crt gene

<400> 4

The <213> response is invalid. Per 1.823 of Sequence Rules, the only valid <213> responses are: "Artificial Sequence," "Unknown," or the Genus/species. FYI: if this is an Artificial Sequence, then "crt gene" would be an insufficient explanation (please explain the source of the genetic material in the <223> response).

Same type of error in sequences 5-16

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

## Validated By CRFValidator v 1.0.2

Application No: 10551508 Version No: 1.0

Input Set:

Output Set:

**Started:** 2007-05-03 16:08:57.906 **Finished:** 2007-05-03 16:08:58.290

Artificial or Unknown found in <213> in SEQ ID (18)

**Elapsed:** 0 hr(s) 0 min(s) 0 sec(s) 384 ms

Total Warnings: 4
Total Errors: 0
No. of SeqIDs Defined: 18
Actual SeqID Count: 18

213

## ErrCode Error Description W 213 Artificial or Unknown found in <213> in SEQ ID (1) W 213 Artificial or Unknown found in <213> in SEQ ID (2) W 213 Artificial or Unknown found in <213> in SEQ ID (17)

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        LEE, Jae Hyung
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Asn Phe Leu Gly Leu Thr Trp Leu Ser Val Gly Leu Phe Phe Ile Ala 55 60

His Asp Ala Met His Gly Ser Val Val Pro Gly Arg Pro Arg Gly Asn 70

Ala Ala Met Gly Gln Leu Val Leu Trp Leu Tyr Ala Gly Phe Ser Trp 85 90

Arg Lys Met Ile Val Lys His Met Ala His His Arg His Thr Gly Thr 100 105 110

Asp Asp Asp Pro Asp Phe Asp His Gly Gly Pro Val Arg Trp Tyr Ala 125 115 120

Arg Phe Ile Gly Thr Tyr Phe Gly Trp Arg Glu Gly Leu Leu Pro 130 135

Val Ile Val Thr Val Tyr Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr 150 155

Val Val Phe Trp Pro Leu Pro Ser Ile Leu Ala Ser Ile Gln Leu Phe

165 170 175

Val Phe Gly Thr Trp Leu Pro His Arg Pro Gly His Asp Ala Phe Pro 185 Asp Arg His Asn Ala Arg Ser Ser Arg Ile Ser Asp Pro Val Ser Leu 200

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Gly Trp His Lys Ser His His Glu Glu His Asp His Ala Leu Glu Lys 35 45

40

Asn Asp Leu Tyr Gly Leu Val Phe Ala Val Ile Ala Thr Val Leu Phe 50 60

Thr Val Gly Trp Ile Trp Ala Pro Val Leu Trp Trp Ile Ala Leu Gly 65 70 75 80

Met Thr Val Tyr Gly Leu Ile Tyr Phe Val Leu His Asp Gly Leu Val $85 \hspace{1.5cm} 90 \hspace{1.5cm} 95$ 

His Gln Arg Trp Pro Phe Arg Tyr Ile Pro Arg Lys Gly Tyr Ala Arg 100 105 110

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Arg Thr

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